

1        **IN THE CLAIMS**

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3            This listing of claims will replace all prior versions, and listings, of claims in the  
4 application:

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6        --1. **(Previously Presented)** A method for analyzing a biological sample using a Fourier  
7 Transform Mass Spectrometer (FTMS), said method comprising the steps of:

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- 9            a.        ionizing a drug-dosed biological sample to produce sample (molecular) ions;
- 10            b.        introducing said ions into an analysis region of said FTMS;
- 11            c.        analyzing said ions to determine the molecular weight and abundance of said ions;
- 12            d.        utilizing said molecular weight to determine the empirical formula of each species  
of said sample; and
- 13            e.        identifying each said species by comparing said empirical formula to a database  
14            of formulas for known molecules.

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16        2. **(Original)** A method according to claim 1, wherein said determining of the molecular weight  
17            is performed with an accuracy sufficient to identify empirical formula of said ions.

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19        3. **(Previously Presented)** A method according to claim 1, wherein said database of known  
20            molecules is updated with said determined empirical formulas.

1       4. (Previously Presented) A method for analyzing a biological sample using a Fourier  
2       Transform Mass Spectrometer (FTMS), said method comprising the steps of:  
3           a. ionizing a drug-dosed biological sample to produce sample (molecular) ions;  
4           b. introducing said ions into an analysis region of said FTMS;  
5           c. analyzing said ions to determine the molecular weight and abundance of said ions;  
6           d. determining the molecular structure of each species by multiple stages of mass  
7           spectrometry; and  
8           e. producing a profile of the sample showing structure and concentration data for  
9       each species.

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11       5. (Original) A method according to claim 4, wherein said determining of the molecular weight  
12       is performed with an accuracy sufficient to identify empirical formula of said ions.

1       6. (**Previously Presented**) A method for analyzing a biological sample using a Fourier  
2       Transform Mass Spectrometer (FTMS), said method comprising the steps of:  
3           a.      ionizing a drug-dosed biological sample to produce sample precursor ions;  
4           b.      introducing said ions into the analysis region of said FTMS;  
5           c.      analyzing said ions to determine the molecular weight, the abundance and the  
6       empirical formula of said ions;  
7           d.      fragmenting said sample precursor ions to produce fragment ions;  
8           e.      determining the molecular weight, the abundance and empirical formula of said  
9       fragment ions;  
10          f.      determining the structure of said fragment ions by comparing said empirical  
11       formulas of said fragment ions to a database of fragments with known structure;  
12          g.      combining said structures of said fragment ions to determine the precursor ion  
13       structure for each species in said sample; and  
14          h.      producing a profile of said sample showing structure and concentration data for  
15       selected species of said sample.

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17       7. (**Original**) A method according to claim 6, wherein said determining of the molecular weight  
18       is performed with an accuracy sufficient to identify empirical formula of said ions.  
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20       8. (**Original**) A method according to claim 6, wherein said fragmenting is performed using  
21       photodissociation.  
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1       9. **(Previously Presented)** A method for analyzing a biological sample utilizing Fourier  
2       Transform Mass Spectrometry (FTMS), said method comprising the steps of:  
3           a.      ionizing polar molecules from a drug-dosed biological sample using positive and  
4       negative electrospray to produce sample (molecular) ions;  
5           b.      introducing said ions into an analysis region of said FTMS;  
6           c.      analyzing said ions to determine the molecular weight and abundance of said ions;  
7           d.      utilizing said molecular weight to determine the empirical formula of each species  
8       of said sample; and  
9           e.      identifying each said species by comparing said empirical formula to a database  
10      of formulas for known molecules.

11  
12      10. **(Original)** A method according to claim 9, wherein said determining of the molecular weight  
13      is performed with an accuracy sufficient to identify empirical formula of said ions.

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15      11. **(Previously Presented)** A method according to claim 9, wherein said database of known  
16      molecules is updated with said determined empirical formulas.

1       12. **(Currently Amended)** A method for analyzing a biological sample utilizing Fourier  
2       Transform Mass Spectrometry (FTMS), said method comprising the steps of:  
3           a.       ionizing non-polar molecules from a drug-dosed biological sample using positive  
4       and negative ion atmospheric pressure chemical ionization to produce sample (molecular)  
5       ions[.];  
6           b.       introducing said ions into an analysis region of said FTMS;  
7           c.       analyzing said ions to determine the molecular weight and abundance of said ions;  
8           d.       utilizing said molecular weight to determine the empirical formula of each species  
9       of said sample; and  
10          e.       identifying each said species by comparing said empirical formula to a database  
11       of formulas for known molecules.

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13       13. **(Original)** A method according to claim 12, wherein said determining of the molecular  
14       weight is performed with an accuracy sufficient to identify empirical formula of said ions.

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16       14. **(Previously Presented)** A method according to claim 12, wherein said database of known  
17       molecules is updated with said determined empirical formulas.

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19       15. **(Previously Presented)** A method according to claim 1, wherein said a drug is injected into  
20       said biological sample to create said drug-dosed biological sample.

1       16. (**Previously Presented**) A method according to claim 1, wherein metabolic products are  
2       detected.

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4       17. (**Previously Presented**) A method according to claim 1, wherein cellular changes of said  
5       drug-dosed biological sample are identified.

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7       18. (**Previously Presented**) A method according to claim 4, wherein said a drug is injected into  
8       said biological sample to create said drug-dosed biological sample.

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10      19. (**Previously Presented**) A method according to claim 4, wherein metabolic products are  
11       detected.

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13      20. (**Previously Presented**) A method according to claim 4, wherein cellular changes of said  
14       drug-dosed biological sample are identified.

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16      21. (**Previously Presented**) A method according to claim 6, wherein said a drug is injected into  
17       said biological sample to create said drug-dosed biological sample.

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19      22. (**Previously Presented**) A method according to claim 6, wherein metabolic products are  
20       detected.

1       23. **(Previously Presented)** A method according to claim 6, wherein cellular changes of said  
2       drug-dosed biological sample are identified.

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4       24. **(Previously Presented)** A method according to claim 9, wherein said a drug is injected into  
5       said biological sample to create said drug-dosed biological sample.

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7       25. **(Previously Presented)** A method according to claim 9, wherein metabolic products are  
8       detected.

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10      26. **(Previously Presented)** A method according to claim 9, wherein cellular changes of said  
11      drug-dosed biological sample are identified.

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13      27. **(Previously Presented)** A method according to claim 12, wherein said a drug is injected into  
14      said biological sample to create said drug-dosed biological sample.

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16      28. **(Previously Presented)** A method according to claim 12, wherein metabolic products are  
17      detected.

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19      29. **(Previously Presented)** A method according to claim 12, wherein cellular changes of said  
20      drug-dosed biological sample are identified.--